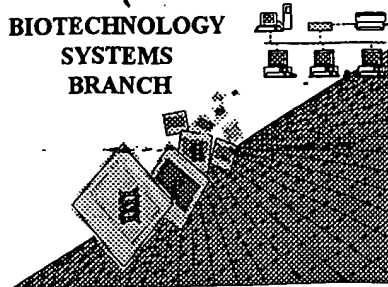


Hines

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



P#10

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/380,826

Source: 1645

Date Processed by STIC: 9/12/2000

RECEIVED
SEP 18 2000
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

J. Hines

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,826

DATE: 09/12/2000
TIME: 12:47:47

Does Not Comply
Corrected Diskette Needed

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\09122000\I380826.raw

SEQUENCE LISTING

- 4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: Agriculture Victoria Services Pty Ltd
7 AND Pig Research and Development Corporation
9 (ii) TITLE OF INVENTION: NOVEL BACTERIAL PATHOGENS
11 (iii) NUMBER OF SEQUENCES: 26
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: DAVIES COLLISON CAVE
15 (B) STREET: 1 LITTLE COLLINS STREET
16 (C) CITY: MELBOURNE
17 (D) STATE: VICTORIA
18 (E) COUNTRY: AUSTRALIA
19 (F) ZIP: 3000
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: US/09/380,826
29 (B) FILING DATE: 22-Nov-1999
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: P05494/97
33 (B) FILING DATE: 07-MAR-97
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: HUGHES E. JOHN L.
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: +61 3 9254 2777
40 (B) TELEFAX: +61 3 9254 2770
41 (C) TELEX: AA 31787

RECEIVED

SEP 18 2000

TECH CENTER 1600/L300

ERRORED SEQUENCES

- 165 (2) INFORMATION FOR SEQ ID NO: 6:
167 (i) SEQUENCE CHARACTERISTICS: 22 short
168 (A) LENGTH: 14 base pairs
169 (B) TYPE: nucleic acid
170 (C) STRANDEDNESS: single
171 (D) TOPOLOGY: linear
173 (ii) MOLECULE TYPE: DNA
175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
E--> 177 TGTGGANNNNNNNTTTGA TA
320 (2) INFORMATION FOR SEQ ID NO: 14:
322 (i) SEQUENCE CHARACTERISTICS: 200 short (next page)
323 (A) LENGTH: 199 base pairs
324 (B) TYPE: nucleic acid

22

RAW SEQUENCE LISTING DATE: 09/12/2000
 PATENT APPLICATION: US/09/380,826 TIME: 12:47:48

Input Set : A:\SEQUENCE LISTING.txt
 Output Set: N:\CRF3\09122000\I380826.raw

```

325          (C) STRANDEDNESS: single
326          (D) TOPOLOGY: linear
OK-> 328      (ii) MOLECULE TYPE: DNA
331      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
333 CCGAGTCTGG GATAACTTTC CGAAAGGGAA GCTAATACTG GATGGTCCCG AGAGATCATA    60
335 AGATTTTTCG GGTAAGATT TATTGCTCGG AGATGAGCCC GCGTCCGATT ASCTAGTTGG    120
337 TGAGGTAAAG GCTCACCAAG GCGACGATCG GTAGCCGGCC TGAGAGGGTG TTCGCCACA    180
E--> 339 ATGGAAGTGA GACACGGTCC    200

363 (2) INFORMATION FOR SEQ ID NO: 16:
365      (i) SEQUENCE CHARACTERISTICS:
366          (A) LENGTH: 28 base pairs 29
367          (B) TYPE: nucleic acid
368          (C) STRANDEDNESS: single
369          (D) TOPOLOGY: linear
OK-> 371      (ii) MOLECULE TYPE: DNA
373      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
E--> 375 CATGGATCCA GAGTTTGATC MTGGCTCAG    29

378 (2) INFORMATION FOR SEQ ID NO: 17:
380      (i) SEQUENCE CHARACTERISTICS:
381          (A) LENGTH: 15 base pairs 16
382          (B) TYPE: nucleic acid
383          (C) STRANDEDNESS: single
384          (D) TOPOLOGY: linear
OK-> 386      (ii) MOLECULE TYPE: DNA
388      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
E--> 390 GTGCCAGCMG CCGCGG    16

393 (2) INFORMATION FOR SEQ ID NO: 18:
395      (i) SEQUENCE CHARACTERISTICS:
396          (A) LENGTH: 18 base pairs 20
397          (B) TYPE: nucleic acid
398          (C) STRANDEDNESS: single
399          (D) TOPOLOGY: linear
OK-> 401      (ii) MOLECULE TYPE: DNA
403      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
E--> 405 AAAGTYAAAK GAATTGACGG    20

438 (2) INFORMATION FOR SEQ ID NO: 21:
440      (i) SEQUENCE CHARACTERISTICS:
441          (A) LENGTH: 14 base pairs 15
442          (B) TYPE: nucleic acid
443          (C) STRANDEDNESS: single
444          (D) TOPOLOGY: linear
WOK 446      (ii) MOLECULE TYPE: DNA
448      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:
E--> 450 ACGGGCGGTG TGTRC    15

467 (2) INFORMATION FOR SEQ ID NO: 23:
469      (i) SEQUENCE CHARACTERISTICS:
470          (A) LENGTH: 16 base pairs 18 (next page)
471          (B) TYPE: nucleic acid
472          (C) STRANDEDNESS: single

```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,826

DATE: 09/12/2000
TIME: 12:47:48

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\09122000\I380826.raw

OK 473 (D) TOPOLOGY: linear
475 (ii) MOLECULE TYPE: DNA
477 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23: 18
E--> 479 GWATTACCGC GGCKGCTG
482 (2) INFORMATION FOR SEQ ID NO: 24:
483 (i) SEQUENCE CHARACTERISTICS: 19
484 (A) LENGTH: 18 base pairs
485 (B) TYPE: nucleic acid
486 (C) STRANDEDNESS: single
487 (D) TOPOLOGY: linear
OK 489 (ii) MOLECULE TYPE: DNA
491 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24: 19
E--> 493 ACCATCATCA CATYGCTGC

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/380,826

DATE: 09/12/2000

TIME: 12:47:49

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF3\09122000\I380826.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:51 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1, Value=[DNA]
L:115 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=2, Value=[DNA]
L:129 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3, Value=[DNA]
L:144 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=4, Value=[DNA]
L:159 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=5, Value=[DNA]
L:173 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=[DNA]
L:177 M:204 E: No. of Bases differ, LENGTH:Input:14 Counted:22 SEQ:6
L:188 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[DNA]
L:203 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8, Value=[DNA]
L:224 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9, Value=[DNA]
L:245 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10, Value=[DNA]
L:266 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11, Value=[DNA]
L:286 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12, Value=[DNA]
L:307 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13, Value=[DNA]
L:328 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14, Value=[DNA]
L:339 M:204 E: No. of Bases differ, LENGTH:Input:199 Counted:200 SEQ:14
L:350 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15, Value=[DNA]
L:371 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=16, Value=[DNA]
L:375 M:204 E: No. of Bases differ, LENGTH:Input:28 Counted:29 SEQ:16
L:386 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=17, Value=[DNA]
L:390 M:204 E: No. of Bases differ, LENGTH:Input:15 Counted:16 SEQ:17
L:401 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=18, Value=[DNA]
L:405 M:204 E: No. of Bases differ, LENGTH:Input:18 Counted:20 SEQ:18
L:416 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=19, Value=[DNA]
L:431 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=20, Value=[DNA]
L:446 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=21, Value=[DNA]
L:450 M:204 E: No. of Bases differ, LENGTH:Input:14 Counted:15 SEQ:21
L:461 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=22, Value=[DNA]
L:475 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=23, Value=[DNA]
L:479 M:204 E: No. of Bases differ, LENGTH:Input:16 Counted:18 SEQ:23
L:489 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24, Value=[DNA]
L:493 M:204 E: No. of Bases differ, LENGTH:Input:18 Counted:19 SEQ:24
L:504 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25, Value=[DNA]
L:519 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=26, Value=[DNA]